Figure 1: 161P2F10B SSH sequence of 182 nucleotides (SEQ. ID. No. 742)

```
  1 GATCACACAT TAGGTTATNG ACTTCAATAT TTTCAAATGG TTCAACTTCA GTCTTCTCTT
 61 TAAAACTGGG TCCATGTGCC AAGAAAGATA GCCTCCATGC TCCTAAACTC ATTGTTATAA
121 CCATGGTTGC CTCCTCCACA ATTTGTATTT GATTTACTCC TAACAGCCAG CCACTGTTGA
181 TC
```

**Figure 2.**

**Figure 2A. The cDNA (SEQ ID. NO. : 744) and amino acid sequence (SEQ ID. NO. : 743) of 161P2F10B.** The 3858 nucleotide sequence of 161P2F10B is shown. The codon for the start methionine is underlined. The open reading frame extends from nucleic acid 44-2671 including the stop codon.

```
   1                                                  M  E  S  T  L  T
   1 ctactttattctgataaaacaggtctatgcagctaccaggacaATGGAATCTACGTTGAC
   7  L  A  T  E  Q  P  V  K  K  N  T  L  K  K  Y  K  I  A  C  I
  61 TTTAGCAACGGAACAACCTGTTAAGAAGAACACTCTTAAGAAATATAAAATAGCTTGCAT
  27  V  L  L  A  L  L  V  I  M  S  L  G  L  G  L  G  L  G  L  R
 121 TGTTCTTCTTGCTTTGCTGGTGATCATGTCACTTGGATTAGGCCTGGGGCTTGGACTCAG
  47  K  L  E  K  Q  G  S  C  R  K  K  C  F  D  A  S  F  R  G  L
 181 GAAACTGGAAAAGCAAGGCAGCTGCAGGAAGAAGTGCTTTGATGCATCATTTAGAGGACT
  67  E  N  C  R  C  D  V  A  C  K  D  R  G  D  C  C  W  D  F  E
 241 GGAGAACTGCCGGTGTGATGTGGCATGTAAAGACCGAGGTGATTGCTGCTGGGATTTTGA
  87  D  T  C  V  E  S  T  R  I  W  M  C  N  K  F  R  C  G  E  T
 301 AGACACCTGTGTGGAATCAACTCGAATATGGATGTGCAATAAATTTCGTTGTGGAGAGAC
 107  R  L  E  A  S  L  C  S  C  S  D  D  C  L  Q  K  K  D  C  C
 361 CAGATTAGAGGCCAGCCTTTGCTCTTGTTCAGATGACTGTTTGCAGAAGAAAGATTGCTG
 127  A  D  Y  K  S  V  C  Q  G  E  T  S  W  L  E  E  N  C  D  T
 421 TGCTGACTATAAGAGTGTTTGCCAAGGAGAAACCTCATGGCTGGAAGAAAACTGTGACAC
 147  A  Q  Q  S  Q  C  P  E  G  F  D  L  P  P  V  I  L  F  S  M
 481 AGCCCAGCAGTCTCAGTGCCCAGAAGGGTTTGACCTGCCACCAGTTATCTTGTTTTCTAT
 167  D  G  F  R  A  E  Y  L  Y  T  W  D  T  L  M  P  N  I  N  K
 541 GGATGGATTTAGAGCTGAATATTTATACACATGGGATACTTTAATGCCAAATATCAATAA
 187  L  K  T  C  G  I  H  S  K  Y  M  R  A  M  Y  P  T  K  T  F
 601 ACTGAAAACATGTGGAATTCATTCAAAATACATGAGAGCTATGTATCCTACCAAAACCTT
 207  P  N  H  Y  T  I  V  T  G  L  Y  P  E  S  H  G  I  I  D  N
 661 CCCAAATCATTACACCATTGTCACGGGCTTGTATCCAGAGTCACATGGCATCATTGACAA
 227  N  M  Y  D  V  N  L  N  K  N  F  S  L  S  S  K  E  Q  N  N
 721 TAATATGTATGATGTAAATCTCAACAAGAATTTTTCACTTTCTTCAAAGGAACAAAATAA
 247  P  A  W  W  H  G  Q  P  M  W  L  T  A  M  Y  Q  G  L  K  A
 781 TCCAGCCTGGTGGCATGGGCAACCAATGTGGCTGACAGCAATGTATCAAGGTTTAAAAGC
 267  A  T  Y  F  W  P  G  S  E  V  A  I  N  G  S  F  P  S  I  Y
 841 CGCTACCTACTTTTGGCCCGGATCAGAAGTGGCTATAAATGGCTCCTTTCCTTCCATATA
 287  M  P  Y  N  G  S  V  P  F  E  E  R  I  S  T  L  L  K  W  L
 901 CATGCCTTACAACGGAAGTGTCCCATTTGAAGAGAGGATTTCTACACTGTTAAAATGGCT
```

307 D L P K A E R P R F Y T M Y F E E P D S

961 GGACCTGCCCAAAGCTGAAAGACCCAGGTTTTATACCATGTATTTTGAAGAACCTGATTC

327 S G H A G G P V S A R V I K A L Q V V D

1021 CTCTGGACATGCAGGTGGACCAGTCAGTGCCAGAGTAATTAAAGCCTTACAGGTAGTAGA

347 H A F G M L M E G L K Q R N L H N C V N

1081 TCATGCTTTTGGGATGTTGATGGAAGGCCTGAAGCAGCGGAATTTGCACAACTGTGTCAA

367 I I L L A D H G M D Q T Y C N K M E Y M

1141 TATCATCCTTCTGGCTGACCATGGAATGGACCAGACTTATTGTAACAAGATGGAATACAT

387 T D Y F P R I N F F Y M Y E G P A P R I

1201 GACTGATTATTTTCCCAGAATAAACTTCTTCTACATGTACGAAGGGCCTGCCCCCCGCAT

407 R A H N I P H D F F S F N S E E I V R N

1261 CCGAGCTCATAATATACCTCATGACTTTTTTAGTTTTAATTCTGAGGAAATTGTTAGAAA

427 L S C R K P D Q H F K P Y L T P D L P K

1321 CCTCAGTTGCCGAAAACCTGATCAGCATTTCAAGCCCTATTTGACTCCTGATTTGCCAAA

447 R L H Y A K N V R I D K V H L F V D Q Q

1381 GCGACTGCACTATGCCAAGAACGTCAGAATCGACAAAGTTCATCTCTTTGTGGATCAACA

467 W L A V R S K S N T N C G G G N H G Y N

1441 GTGGCTGGCTGTTAGGAGTAAATCAAATACAAATTGTGGAGGAGGCAACCATGGTTATAA

487 N E F R S M E A I F L A H G P S F K E K

1501 CAATGAGTTTAGGAGCATGGAGGCTATCTTTCTGGCACATGGACCCAGTTTTAAAGAGAA

507 T E V E P F E N I E V Y N L M C D L L R

1561 GACTGAAGTTGAACCATTTGAAAATATTGAAGTCTATAACCTAATGTGTGATCTTCTACG

527 I Q P A P N N G T H G S L N H L L K V P

1621 CATTCAACCAGCACCAAACAATGGAACCCATGGTAGTTTAAACCATCTTCTGAAGGTGCC

547 F Y E P S H A E E V S K F S V C G F A N

1681 TTTTTATGAGCCATCCCATGCAGAGGAGGTGTCAAAGTTTTCTGTTTGTGGCTTTGCTAA

567 P L P T E S L D C F C P H L Q N S T Q L

1741 TCCATTGCCCACAGAGTCTCTTGACTGTTTCTGCCCTCACCTACAAAATAGTACTCAGCT

587 E Q V N Q M L N L T Q E E I T A T V K V

1801 GGAACAAGTGAATCAGATGCTAAATCTCACCCAAGAAGAAATAACAGCAACAGTGAAAGT

607 N L P F G R P R V L Q K N V D H C L L Y

1861 AAATTTGCCATTTGGGAGGCCTAGGGTACTGCAGAAGAACGTGGACCACTGTCTCCTTTA

627 H R E Y V S G F G K A M R M P M W S S Y

1921 CCACAGGGAATATGTCAGTGGATTTGGAAAAGCTATGAGGATGCCCATGTGGAGTTCATA

647 T V P Q L G D T S P L P P T V P D C L R

1981 CACAGTCCCCCAGTTGGGAGACACATCGCCTCTGCCTCCCACTGTCCCAGACTGTCTGCG

667 A D V R V P P S E S Q K C S F Y L A D K

2041 GGCTGATGTCAGGGTTCCTCCTTCTGAGAGCCAAAAATGTTCCTTCTATTTAGCAGACAA

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 687  N  I  T  H  G  F  L  Y  P  P  A  S  N  R  T  S  D  S  Q  Y
2101 GAATATCACCCACGGCTTCCTCTATCCTCCTGCCAGCAATAGAACATCAGATAGCCAATA
 707  D  A  L  I  T  S  N  L  V  P  M  Y  E  E  F  R  K  M  W  D
2161 TGATGCTTTAATTACTAGCAATTTGGTACCTATGTATGAAGAATTCAGAAAAATGTGGGA
 727  Y  F  H  S  V  L  L  I  K  H  A  T  E  R  N  G  V  N  V  V
2221 CTACTTCCACAGTGTTCTTCTTATAAAACATGCCACAGAAAGAAATGGAGTAAATGTGGT
 747  S  G  P  I  F  D  Y  N  Y  D  G  H  F  D  A  P  D  E  I  T
2281 TAGTGGACCAATATTTGATTATAATTATGATGGCCATTTTGATGCTCCAGATGAAATTAC
 767  K  H  L  A  N  T  D  V  P  I  P  T  H  Y  F  V  V  L  T  S
2341 CAAACATTTAGCCAACACTGATGTTCCCATCCCAACACACTACTTTGTGGTGCTGACCAG
 787  C  K  N  K  S  H  T  P  E  N  C  P  G  W  L  D  V  L  P  F
2401 TTGTAAAAACAAGAGCCACACACCGGAAAACTGCCCTGGGTGGCTGGATGTCCTACCCTT
 807  I  I  P  H  R  P  T  N  V  E  S  C  P  E  G  K  P  E  A  L
2461 TATCATCCCTCACCGACCTACCAACGTGGAGAGCTGTCCTGAAGGTAAACCAGAAGCTCT
 827  W  V  E  E  R  F  T  A  H  I  A  R  V  R  D  V  E  L  L  T
2521 TTGGGTTGAAGAAAGATTTACAGCTCACATTGCCCGGGTCCGTGATGTAGAACTTCTCAC
 847  G  L  D  F  Y  Q  D  K  V  Q  P  V  S  E  I  L  Q  L  K  T
2581 TGGGCTTGACTTCTATCAGGATAAAGTGCAGCCTGTCTCTGAAATTTTGCAACTAAAGAC
 867  Y  L  P  T  F  E  T  T  I  *
2641 ATATTTACCAACATTTGAAACCACTATTTAActtaataatgtctacttaatatataatttt
2701 actgtataaagtaattttggcaaaatataagtgatttttctggagaattgtaaaataaa
2761 gttttctatttttccttaaaaaaaaaaccggaattccgggcttgggaggctgaggcagga
2821 gactcgcttgaacccgggaggcagaggttgcagtgagccaagattgcgccattgcactcc
2881 agagcctgggtgacagagcaagactacatctcaaaaaataaataaataaaataaaagtaa
2941 caataaaaataaaaagaacagcagagagaatgagcaaggagaaatgtcacaaactattgc
3001 aaaatactgttacactgggttggctctccaagaagatactggaatctcttcagccatttg
3061 cttttcagaagtagaaaccagcaaaccacctctaagcggagaacatacgattctttatta
3121 agtagctctggggaaggaaagaataaaagttgatagctccctgattgggaaaaaatgcac
3181 aattaataaagaatgaagatgaaagaaagcatgcttatgttgtaacacaaaaaaaattca
3241 caaacgttggtggaaggaaaacagtatagaaaacattactttaactaaaagctggaaaaa
3301 ttttcagttgggatgcgactgacaaaaagaacgggatttccaggcataaagttggcgtga
3361 gctacagagggcaccatgtggctcagtggaagacccttcaagattcaaagttccatttga
3421 cagagcaaaggcacttcgcaaggagaagggtttaaattatgggtccaaaagccaagtggt
3481 aaagcgagcaatttgcagcataactgcttctcctagacagggctgagtgggcaaaatacg
3541 acagtacacacagtgactattagccactgccagaaacaggctgaacagccctgggagaca
3601 agggaaggcaggtggtgggagttgttcatggagagaaaggagagttttagaaccagcaca
3661 tccactggagatgctgggccaccagacccctcccagtcaataaagtctggtgcctcattt
3721 gatctcagcctcatcatgaccctggagagaccctgataccatctgccagtccccgacagc
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3781 ttaggcactccttgccatcaacctgacccccgagtggttctccaggctccctgccccac
3841 ccattcaggccggaattc
```

**Figure 2B: The cDNA (SEQ ID. NO. : 746) and amino acid sequence (SEQ ID. NO. : 745) of 161P2F10B variant 1.** The 3858 nucleotide sequence of 161P2F10B variant 1 is shown. The start methionine is underlined. The open reading frame extends from nucleic acid 44-2671 including the stop codon.

```
   1                                                M  E  S  T  L  T
   1 ctactttattctgataaaacaggtctatgcagctaccaggacaATGGAATCTACGTTGAC
   7  L  A  T  E  Q  P  V  K  K  N  T  L  K  K  Y  K  I  A  C  I
  61 TTTAGCAACGGAACAACCTGTTAAGAAGAACACTCTTAAGAAATATAAAATAGCTTGCAT
  27  V  L  L  A  L  L  V  I  M  S  L  G  L  G  L  G  L  G  L  R
 121 TGTTCTTCTTGCTTTGCTGGTGATCATGTCACTTGGATTAGGCCTGGGGCTTGGACTCAG
  47  K  L  E  K  Q  G  S  C  R  K  K  C  F  D  A  S  F  R  G  L
 181 GAAACTGGAAAAGCAAGGCAGCTGCAGGAAGAAGTGCTTTGATGCATCATTTAGAGGACT
  67  E  N  C  R  C  D  V  A  C  K  D  R  G  D  C  C  W  D  F  E
 241 GGAGAACTGCCGGTGTGATGTGGCATGTAAAGACCGAGGTGATTGCTGCTGGGATTTTGA
  87  D  T  C  V  E  S  T  R  I  W  M  C  N  K  F  R  C  G  E  T
 301 AGACACCTGTGTGGAATCAACTCGAATATGGATGTGCAATAAATTTCGTTGTGGAGAGAC
 107  R  L  E  A  S  L  C  S  C  S  D  D  C  L  Q  R  K  D  C  C
 361 CAGATTAGAGGCCAGCCTTTGCTCTTGTTCAGATGACTGTTTGCAGAGGAAAGATTGCTG
 127  A  D  Y  K  S  V  C  Q  G  E  T  S  W  L  E  E  N  C  D  T
 421 TGCTGACTATAAGAGTGTTTGCCAAGGAGAAACCTCATGGCTGGAAGAAAACTGTGACAC
 147  A  Q  Q  S  Q  C  P  E  G  F  D  L  P  P  V  I  L  F  S  M
 481 AGCCCAGCAGTCTCAGTGCCCAGAAGGGTTTGACCTGCCACCAGTTATCTTGTTTTCTAT
 167  D  G  F  R  A  E  Y  L  Y  T  W  D  T  L  M  P  N  I  N  K
 541 GGATGGATTTAGAGCTGAATATTTATACACATGGGATACTTTAATGCCAAATATCAATAA
 187  L  K  T  C  G  I  H  S  K  Y  M  R  A  M  Y  P  T  K  T  F
 601 ACTGAAAACATGTGGAATTCATTCAAAATACATGAGAGCTATGTATCCTACCAAAACCTT
 207  P  N  H  Y  T  I  V  T  G  L  Y  P  E  S  H  G  I  I  D  N
 661 CCCAAATCATTACACCATTGTCACGGGCTTGTATCCAGAGTCACATGGCATCATTGACAA
 227  N  M  Y  D  V  N  L  N  K  N  F  S  L  S  S  K  E  Q  N  N
 721 TAATATGTATGATGTAAATCTCAACAAGAATTTTTCACTTTCTTCAAAGGAACAAAATAA
 247  P  A  W  W  H  G  Q  P  M  W  L  T  A  M  Y  Q  G  L  K  A
 781 TCCAGCCTGGTGGCATGGGCAACCAATGTGGCTGACAGCAATGTATCAAGGTTTAAAAGC
 267  A  T  Y  F  W  P  G  S  E  V  A  I  N  G  S  F  P  S  I  Y
 841 CGCTACCTACTTTTGGCCCGGATCAGAAGTGGCTATAAATGGCTCCTTTCCTTCCATATA
```

287 M P Y N G S V P F E E R I S T L L K W L

901 CATGCCTTACAACGGAAGTGTCCCATTTGAAGAGAGGATTTCTACACTGTTAAAATGGCT

307 D L P K A E R P R F Y T M Y F E E P D S

961 GGACCTGCCCAAAGCTGAAAGACCCAGGTTTTATACCATGTATTTTGAAGAACCTGATTC

327 S G H A G G P V S A R V I K A L Q V V D

1021 CTCTGGACATGCAGGTGGACCAGTCAGTGCCAGAGTAATTAAAGCCTTACAGGTAGTAGA

347 H A F G M L M E G L K Q R N L H N C V N

1081 TCATGCTTTTGGGATGTTGATGGAAGGCCTGAAGCAGCGGAATTTGCACAACTGTGTCAA

367 I I L L A D H G M D Q T Y C N K M E Y M

1141 TATCATCCTTCTGGCTGACCATGGAATGGACCAGACTTATTGTAACAAGATGGAATACAT

387 T D Y F P R I N F F Y M Y E G P A P R I

1201 GACTGATTATTTTCCCAGAATAAACTTCTTCTACATGTACGAAGGGCCTGCCCCCCGCAT

407 R A H N I P H D F F S F N S E E I V R N

1261 CCGAGCTCATAATATACCTCATGACTTTTTTAGTTTTAATTCTGAGGAAATTGTTAGAAA

427 L S C R K P D Q H F K P Y L T P D L P K

1321 CCTCAGTTGCCGAAAACCTGATCAGCATTTCAAGCCCTATTTGACTCCTGATTTGCCAAA

447 R L H Y A K N V R I D K V H L F V D Q Q

1381 GCGACTGCACTATGCCAAGAACGTCAGAATCGACAAAGTTCATCTCTTTGTGGATCAACA

467 W L A V R S K S N T N C G G G N H G Y N

1441 GTGGCTGGCTGTTAGGAGTAAATCAAATACAAATTGTGGAGGAGGCAACCATGGTTATAA

487 N E F R S M E A I F L A H G P S F K E K

1501 CAATGAGTTTAGGAGCATGGAGGCTATCTTTCTGGCACATGGACCCAGTTTTAAAGAGAA

507 T E V E P F E N I E V Y N L M C D L L R

1561 GACTGAAGTTGAACCATTTGAAAATATTGAAGTCTATAACCTAATGTGTGATCTTCTACG

527 I Q P A P N N G T H G S L N H L L K V P

1621 CATTCAACCAGCACCAAACAATGGAACCCATGGTAGTTTAAACCATCTTCTGAAGGTGCC

547 F Y E P S H A E E V S K F S V C G F A N

1681 TTTTTATGAGCCATCCCATGCAGAGGAGGTGTCAAAGTTTTCTGTTTGTGGCTTTGCTAA

567 P L P T E S L D C F C P H L Q N S T Q L

1741 TCCATTGCCCACAGAGTCTCTTGACTGTTTCTGCCCTCACCTACAAAATAGTACTCAGCT

587 E Q V N Q M L N L T Q E E I T A T V K V

1801 GGAACAAGTGAATCAGATGCTAAATCTCACCCAAGAAGAAATAACAGCAACAGTGAAAGT

607 N L P F G R P R V L Q K N V D H C L L Y

1861 AAATTTGCCATTTGGGAGGCCTAGGGTACTGCAGAAGAACGTGGACCACTGTCTCCTTTA

627 H R E Y V S G F G K A M R M P M W S S Y

1921 CCACAGGGAATATGTCAGTGGATTTGGAAAAGCTATGAGGATGCCCATGTGGAGTTCATA

647 T V P Q L G D T S P L P P T V P D C L R

1981 CACAGTCCCCCAGTTGGGAGACACATCGCCTCTGCCTCCCACTGTCCCAGACTGTCTGCG

667 A D V R V P P S E S Q K C S F Y L A D K

2041 GGCTGATGTCAGGGTTCCTCCTTCTGAGAGCCAAAAATGTTCCTTCTATTTAGCAGACAA

687 N I T H G F L Y P P A S N R T S D S Q Y

2101 GAATATCACCCACGGCTTCCTCTATCCTCCTGCCAGCAATAGAACATCAGATAGCCAATA

707 D A L I T S N L V P M Y E E F R K M W D

2161 TGATGCTTTAATTACTAGCAATTTGGTACCTATGTATGAAGAATTCAGAAAAATGTGGGA

727 Y F H S V L L I K H A T E R N G V N V V

2221 CTACTTCCACAGTGTTCTTCTTATAAAACATGCCACAGAAAGAAATGGAGTAAATGTGGT

747 S G P I F D Y N Y D G H F D A P D E I T

2281 TAGTGGACCAATATTTGATTATAATTATGATGGCCATTTTGATGCTCCAGATGAAATTAC

767 K H L A N T D V P I P T H Y F V V L T S

2341 CAAACATTTAGCCAACACTGATGTTCCCATCCCAACACACTACTTTGTGGTGCTGACCAG

787 C K N K S H T P E N C P G W L D V L P F

2401 TTGTAAAAACAAGAGCCACACACCGGAAAACTGCCCTGGGTGGCTGGATGTCCTACCCTT

807 I I P H R P T N V E S C P E G K P E A L

2461 TATCATCCCTCACCGACCTACCAACGTGGAGAGCTGTCCTGAAGGTAAACCAGAAGCTCT

827 W V E E R F T A H I A R V R D V E L L T

2521 TTGGGTTGAAGAAAGATTTACAGCTCACATTGCCCGGGTCCGTGATGTAGAACTTCTCAC

847 G L D F Y Q D K V Q P V S E I L Q L K T

2581 TGGGCTTGACTTCTATCAGGATAAAGTGCAGCCTGTCTCTGAAATTTTGCAACTAAAGAC

867 Y L P T F E T T I *

2641 ATATTTACCAACATTTGAAACCACTATTTAActtaataatgtctacttaatatataattt

2701 actgtataaagtaatttggcaaaatataagtgatttttctggagaattgtaaaataaa

2761 gttttctatttttccttaaaaaaaaaaccggaattccgggcttgggaggctgaggcagga

2821 gactcgcttgaacccgggaggcagaggttgcagtgagccaagattgcgccattgcactcc

2881 agagcctgggtgacagagcaagactacatctcaaaaaataaataaataaaataaaagtaa

2941 caataaaaataaaaagaacagcagagagaatgagcaaggagaaatgtcacaaactattgc

3001 aaaatactgttacactgggttggctctccaagaagatactggaatctcttcagccatttg

3061 cttttcagaagtagaaaccagcaaaccacctctaagcggagaacatacgattctttatta

3121 agtagctctggggaaggaaagaataaaagttgatagctccctgattgggaaaaaatgcac

3181 aattaataaagaatgaagatgaaagaaagcatgcttatgttgtaacacaaaaaaaattca

3241 caaacgttggtggaaggaaaacagtatagaaaacattactttaactaaaagctggaaaaa

3301 ttttcagttgggatgcgactgacaaaaagaacgggatttccaggcataaagttggcgtga

3361 gctacagagggcaccatgtggctcagtggaagacccttcaagattcaaagttccatttga

3421 cagagcaaaggcacttcgcaaggagaagggtttaaattatgggtccaaaagccaagtggt

3481 aaagcgagcaatttgcagcataactgcttctcctagacagggctgagtgggcaaaatacg

3541 acagtacacacagtgactattagccactgccagaaacaggctgaacagccctgggagaca

3601 agggaaggcaggtggtgggagttgttcatggagagaaaggagagttttagaaccagcaca

3661 tccactggagatgctgggccaccagacccctcccagtcaataaagtctggtgcctcattt

3721 gatctcagcctcatcatgaccctggagagaccctgataccatctgccagtccccgacagc

3781 ttaggcactccttgccatcaacctgacccccgagtggttctccaggctccctgccccac

3841 ccattcaggccggaattc

**Figure 3A. Amino acid sequence of 161P2F10B (SEQ ID. NO. : 747).** The 161P2F10B protein has 875 amino acids.

```
  1 MESTLTLATE QPVKKNTLKK YKIACIVLLA LLVIMSLGLG LGLGLRKLEK QGSCRKKCFD
 61 ASFRGLENCR CDVACKDRGD CCWDFEDTCV ESTRIWMCNK FRCGETRLEA SLCSCSDDCL
121 QKKDCCADYK SVCQGETSWL EENCDTAQQS QCPEGFDLPP VILFSMDGFR AEYLYTWDTL
181 MPNINKLKTC GIHSKYMRAM YPTKTFPNHY TIVTGLYPES HGIIDNNMYD VNLNKNFSLS
241 SKEQNNPAWW HGQPMWLTAM YQGLKAATYF WPGSEVAING SFPSIYMPYN GSVPFEERIS
301 TLLKWLDLPK AERPRFYTMY FEEPDSSGHA GGPVSARVIK ALQVVDHAFG MLMEGLKQRN
361 LHNCVNIILL ADHGMDQTYC NKMEYMTDYF PRINFFYMYE GPAPRIRAHN IPHDFFSFNS
421 EEIVRNLSCR KPDQHFKPYL TPDLPKRLHY AKNVRIDKVH LFVDQQWLAV RSKSNTNCGG
481 GNHGYNNEFR SMEAIFLAHG PSFKEKTEVE PFENIEVYNL MCDLLRIQPA PNNGTHGSLN
541 HLLKVPFYEP SHAEEVSKFS VCGFANPLPT ESLDCFCPHL QNSTQLEQVN QMLNLTQEEI
601 TATVKVNLPF GRPRVLQKNV DHCLLYHREY VSGFGKAMRM PMWSSYTVPQ LGDTSPLPPT
661 VPDCLRADVR VPPSESQKCS FYLADKNITH GFLYPPASNR TSDSQYDALI TSNLVPMYEE
721 FRKMWDYFHS VLLIKHATER NGVNVVSGPI FDYNYDGHFD APDEITKHLA NTDVPIPTHY
781 FVVLTSCKNK SHTPENCPGW LDVLPFIIPH RPTNVESCPE GKPEALWVEE RFTAHIARVR
841 DVELLTGLDF YQDKVQPVSE ILQLKTYLPT FETTI
```

**Figure 3B. Amino acid sequence of 161P2F10B variant 1 (SEQ ID. NO. : 748).** The 161P2F10B variant 1 protein has 875 amino acids.

```
  1 MESTLTLATE QPVKKNTLKK YKIACIVLLA LLVIMSLGLG LGLGLRKLEK QGSCRKKCFD
 61 ASFRGLENCR CDVACKDRGD CCWDFEDTCV ESTRIWMCNK FRCGETRLEA SLCSCSDDCL
121 QRKDCCADYK SVCQGETSWL EENCDTAQQS QCPEGFDLPP VILFSMDGFR AEYLYTWDTL
181 MPNINKLKTC GIHSKYMRAM YPTKTFPNHY TIVTGLYPES HGIIDNNMYD VNLNKNFSLS
241 SKEQNNPAWW HGQPMWLTAM YQGLKAATYF WPGSEVAING SFPSIYMPYN GSVPFEERIS
301 TLLKWLDLPK AERPRFYTMY FEEPDSSGHA GGPVSARVIK ALQVVDHAFG MLMEGLKQRN
361 LHNCVNIILL ADHGMDQTYC NKMEYMTDYF PRINFFYMYE GPAPRIRAHN IPHDFFSFNS
421 EEIVRNLSCR KPDQHFKPYL TPDLPKRLHY AKNVRIDKVH LFVDQQWLAV RSKSNTNCGG
481 GNHGYNNEFR SMEAIFLAHG PSFKEKTEVE PFENIEVYNL MCDLLRIQPA PNNGTHGSLN
541 HLLKVPFYEP SHAEEVSKFS VCGFANPLPT ESLDCFCPHL QNSTQLEQVN QMLNLTQEEI
601 TATVKVNLPF GRPRVLQKNV DHCLLYHREY VSGFGKAMRM PMWSSYTVPQ LGDTSPLPPT
661 VPDCLRADVR VPPSESQKCS FYLADKNITH GFLYPPASNR TSDSQYDALI TSNLVPMYEE
721 FRKMWDYFHS VLLIKHATER NGVNVVSGPI FDYNYDGHFD APDEITKHLA NTDVPIPTHY
781 FVVLTSCKNK SHTPENCPGW LDVLPFIIPH RPTNVESCPE GKPEALWVEE RFTAHIARVR
841 DVELLTGLDF YQDKVQPVSE ILQLKTYLPT FETTI
```

**Figure 4**

**Figure 4A. Amino acid alignment of 161P2F10B (SEQ. ID. No. 747) with ENPP3 (SEQ. ID. No. 765).**

```
161P2F10B  mestltlateqpvkkntlkkykiacivllallvimslglg  40
   ENPP3   mestltlateqpvkkntlkkykiacivllallvimslglg  40

161P2F10B  lglglrklekqgscrkkcfdasfrglencrcdvackdrgd  80
   ENPP3   lglglrklekqgscrkkcfdasfrglencrcdvackdrgd  80

161P2F10B  ccwdfedtcvestriwmcnkfrcgetrleaslcscsddcl  120
   ENPP3   ccwdfedtcvestriwmcnkfrcgetrleaslcscsddcl  120

161P2F10B  qkkdccadyksvcqgetswleencdtaqqsqcpegfdlpp  160
   ENPP3   qkkdccadyksvcqgetswleencdtaqqsqcpegfdlpp  160

161P2F10B  vilfsmdgfraeylytwdtlmpninklktcgihskymram  200
   ENPP3   vilfsmdgfraeylytwdtlmpninklktcgihskymram  200

161P2F10B  yptktfpnhytivtglypeshgiidnnmydvnlnknfsls  240
   ENPP3   yptktfpnhytivtglypeshgiidnnmydvnlnknfsls  240

161P2F10B  skeqnnpawwhgqpmwltamyqglkaatyfwpgsevaing  280
   ENPP3   skeqnnpawwhgqpmwltamyqglkaatyfwpgsevaing  280

161P2F10B  sfpsiympyngsvpfeeristllkwldlpkaerprfytmy  320
   ENPP3   sfpsiympyngsvpfeeristllkwldlpkaerprfytmy  320

161P2F10B  feepdssghaggpvsarvikalqvvdhafgmlmeglkqrn  360
   ENPP3   feepdssghaggpvsarvikalqvvdhafgmlmeglkqrn  360

161P2F10B  lhncvniilladhgmdqtycnkmeymtdyfprinffymye  400
   ENPP3   lhnrvniilladhgmdqtycnkmeymtdyfprinffymye  400

161P2F10B  gpaprirahniphdffsfnseeivrnlscrkpdqhfkpyl  440
   ENPP3   gpaprirahniphdffsfnseeivrnlscrkpdqhfkpyl  440

161P2F10B  tpdlpkrlhyaknvridkvhlfvdqqwlavrsksntncgg  480
   ENPP3   tpdlpkrlhyaknvridkvhlfvdqqwlavrsksntncgg  480
```

```
161P2F10B  gnhgynnefrsmeaiflahgpsfkektevepfenievynl  520
   ENPP3   gnhgynnefrsmeaiflahgpsfkektevepfenievynl  520

161P2F10B  mcdllriqpapnngthgslnhllkvpfyepshaeevskfs  560
   ENPP3   mcdllriqpapnngthgslnhllkvpfyepshaeevskfs  560

161P2F10B  vcgfanplptesldcfcphlqnstqleqvnqmlnltqeei  600
   ENPP3   vcgfanplptesldcfcphlqnstqleqvnqmlnltqeei  600

161P2F10B  tatvkvnlpfgrprvlqknvdhcllyhreyvsgfgkamrm  640
   ENPP3   tatvkvnlpfgrprvlqknvdhcllyhreyvsgfgkamrm  640

161P2F10B  pmwssytvpqlgdtsplpptvpdclradvrvppsesqkcs  680
   ENPP3   pmwssytvpqlgdtsplpptvpdclradvrvppsesqkcs  680

161P2F10B  fyladknithgflyppasnrtsdsqydalitsnlvpmyee  720
   ENPP3   fyladknithgflyppasnrtsdsqydalitsnlvpmyee  720

161P2F10B  frkmwdyfhsvllikhaternqvnvvsgpifdynydghfd  760
   ENPP3   frkmwdyfhsvllikhaternqvnvvsgpifdynydghfd  760

161P2F10B  apdeitkhlantdvpiptnyfvvltsckqkshtpencpgw  800
   ENPP3   apdeitkhlantdvpiptnyfvvltsckqkshtpencpgw  800

161P2F10B  ldvlpfiiphrptnvescpegkpealwveerftahiarvr  840
   ENPP3   ldvlpfiiphrptnvescpegkpealwveerftahiarvr  840

161P2F10B  dvelltgldfyqdkvqpvseilqlktylptfetti      875
   ENPP3   dvelltgldfyqdkvqpvseilqlktylptfetti      875
```

**Figure 4b. Amino acid alignment of 161P2F10B (SEQ. ID. No. 747) with 161P2F10B variant 1 (SEQ. ID. No. 748).**

```
          161P2F10B  mestltlateqpvkkntlkkykiacivllallvimslglg  40
161P2F10B variant 1  mestltlateqpvkkntlkkykiacivllallvimslglg  40

          161P2F10B  lglglrklekqgscrkkcfdasfrglencrcdvackdrgd  80
161P2F10B variant 1  lglglrklekqgscrkkcfdasfrglencrcdvackdrgd  80
```

```
          161P2F10B  ccwdfedtcvestriwmcnkfrcgetrleaslcscsddcl  120
161P2F10B variant 1  ccwdfedtcvestriwmcnkfrcgetrleaslcscsddcl  120

          161P2F10B  qkkdccadyksvcqgetswleencdtaqqsqcpegfdlpp  160
161P2F10B variant 1  qrkdccadyksvcqgetswleencdtaqqsqcpegfdlpp  160

          161P2F10B  vilfsmdgfraeylytwdtlmpninklktcgihskymram  200
161P2F10B variant 1  vilfsmdgfraeylytwdtlmpninklktcgihskymram  200

          161P2F10B  yptktfpnhytivtglypeshgiidnnmydvnlnknfsls  240
161P2F10B variant 1  yptktfpnhytivtglypeshgiidnnmydvnlnknfsls  240

          161P2F10B  skeqnnpawwhgqpmwltamyqglkaatyfwpgsevaing  280
161P2F10B variant 1  skeqnnpawwhgqpmwltamyqglkaatyfwpgsevaing  280

          161P2F10B  sfpsiympyngsvpfeeristllkwldlpkaerprfytmy  320
161P2F10B variant 1  sfpsiympyngsvpfeeristllkwldlpkaerprfytmy  320

          161P2F10B  feepdssghaggpvsarvikalqvvdhafgmlmeglkqrn  360
161P2F10B variant 1  feepdssghaggpvsarvikalqvvdhafgmlmeglkqrn  360

          161P2F10B  lhncvniilladhgmdqtycnkmeymtdyfprinffymye  400
161P2F10B variant 1  lhnrvniilladhgmdqtycnkmeymtdyfprinffymye  400

          161P2F10B  gpapriranhniphdffsfnseeivrnlscrkpdqhfkpyl  440
161P2F10B variant 1  gpapriranhniphdffsfnseeivrnlscrkpdqhfkpyl  440

          161P2F10B  tpdlpkrlhyaknvridkvhlfvdqqwlavrsksntncgg  480
161P2F10B variant 1  tpdlpkrlhyaknvridkvhlfvdqqwlavrsksntncgg  480

          161P2F10B  gnhgynnefrsmeaiflahgpsfkektevepfenievynl  520
161P2F10B variant 1  gnhgynnefrsmeaiflahgpsfkektevepfenievynl  520

          161P2F10B  mcdllriqppapnngthgslnhllkvpfyepshaeevskfs  560
161P2F10B variant 1  mcdllriqppapnngthgslnhllkvpfyepshaeevskfs  560

          161P2F10B  vcgfanplptesldcfcphlqnstqleqvnqmlnltqeei  600
161P2F10B variant 1  vcgfanplptesldcfcphlqnstqleqvnqmlnltqeei  600
```

```
          161P2F10B  t a t v k v n l p f g r p r v l q k n v d h c l l y h r e y v s g f g k a m r m  640
161P2F10B variant 1  t a t v k v n l p f g r p r v l q k n v d h c l l y h r e y v s g f g k a m r m  640

          161P2F10B  p m w s s y t v p q l g d t s p l p p t v p d c l r a d v r v p p s e s q k c s  680
161P2F10B variant 1  p m w s s y t v p q l g d t s p l p p t v p d c l r a d v r v p p s e s q k c s  680

          161P2F10B  f y l a d k n i t h g f l y p p a s n r t s d s q y d a l i t s n l v p m y e e  720
161P2F10B variant 1  f y l a d k n i t h g f l y p p a s n r t s d s q y d a l i t s n l v p m y e e  720

          161P2F10B  f r k m w d y f h s v l l i k h a t e r n g v n v v s g p i f d y n y d g h f d  760
161P2F10B variant 1  f r k m w d y f h s v l l i k h a t e r n g v n v v s g p i f d y n y d g h f d  760

          161P2F10B  a p d e i t k h l a n t d v p i p t h y f v v l t s c k n k s h t p e n c p g w  800
161P2F10B variant 1  a p d e i t k h l a n t d v p i p t h y f v v l t s c k n k s h t p e n c p g w  800

          161P2F10B  l d v l p f i i p h r p t n v e s c p e g k p e a l w v e e r f t a h i a r v r  840
161P2F10B variant 1  l d v l p f i i p h r p t n v e s c p e g k p e a l w v e e r f t a h i a r v r  840

          161P2F10B  d v e l l t g l d f y q d k v q p v s e i l q l k t y l p t f e t t i        875
161P2F10B variant 1  d v e l l t g l d f y q d k v q p v s e i l q l k t y l p t f e t t i        875
```

**4C) Alignment of 161P2F10B (SEQ. ID. No. 749) and SNP variant 2 (SEQ. ID. No. 750) carrying a T to P mutation at position 874.**

```
Query: 492 MEAIFLAHGPSFKEKTEVEPFENIEVYNLMCDLLRIQPAPNNGTHGSLNHLLKVPFYEPS 551
           MEAIFLAHGPSFKEKTEVEPFENIEVYNLMCDLLRIQPAPNNGTHGSLNHLLKVPFYEPS
Sbjct: 1   MEAIFLAHGPSFKEKTEVEPFENIEVYNLMCDLLRIQPAPNNGTHGSLNHLLKVPFYEPS 60

Query: 552 HAEEVSKFSVCGFANPLPTESLDCFCPHLQNSTQLEQVNQMLNLTQEEITATVKVNLPFG 611
           HAEEVSKFSVCGFANPLPTESLDCFCPHLQNSTQLEQVNQMLNLTQEEITATVKVNLPFG
Sbjct: 61  HAEEVSKFSVCGFANPLPTESLDCFCPHLQNSTQLEQVNQMLNLTQEEITATVKVNLPFG 120

Query: 612 RPRVLQKNVDHCLLYHREYVSGFGKAMRMPMWSSYTVPQLGDTSPLPPTVPDCLRADVRV
671
           RPRVLQKNVDHCLLYHREYVSGFGKAMRMPMWSSYTVPQLGDTSPLPPTVPDCLRADVRV
Sbjct: 121 RPRVLQKNVDHCLLYHREYVSGFGKAMRMPMWSSYTVPQLGDTSPLPPTVPDCLRADVRV 180

Query: 672 PPSESQKCSFYLADKNITHGFLYPPASNRTSDSQYDALITSNLVPMYEEFRKMWDYFHSV 731
           PPSESQKCSFYLADKNITHGFLYPPASNRTSDSQYDALITSNLVPMYEEFRKMWDYFHSV
Sbjct: 181 PPSESQKCSFYLADKNITHGFLYPPASNRTSDSQYDALITSNLVPMYEEFRKMWDYFHSV 240

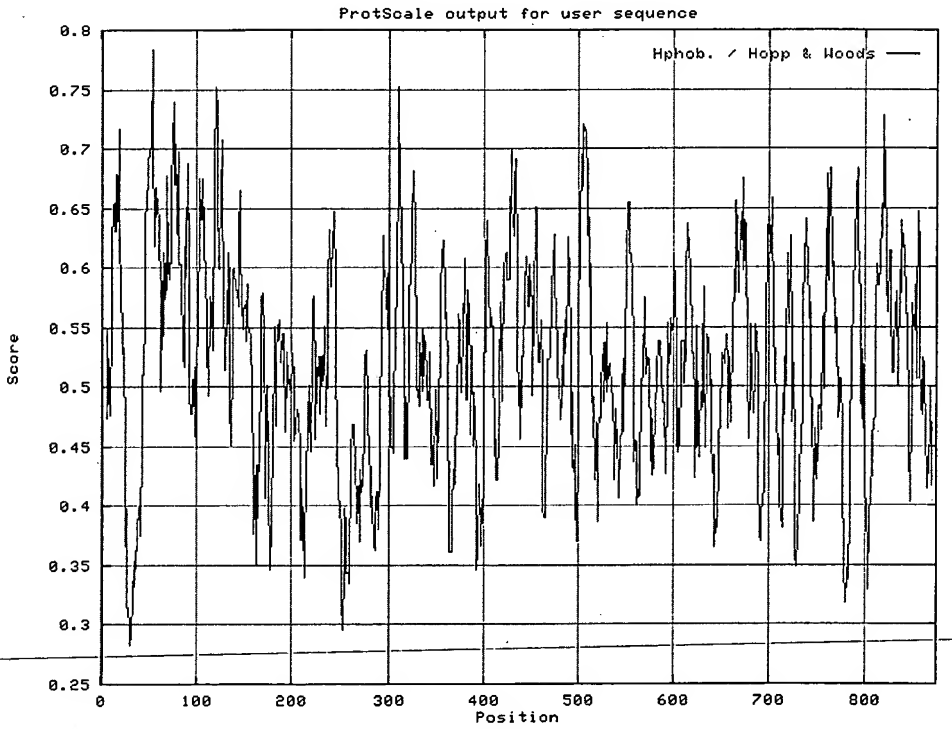
Query: 732 LLIKHATERNGVNVVSGPIFDYNYDGHFDAPDEITKHLANTDVPIPTHYFVVLTSCKNKS 791
           LLIKHATERNGVNVVSGPIFDYNYDGHFDAPDEITKHLANTDVPIPTHYFVVLTSCKNKS
Sbjct: 241 LLIKHATERNGVNVVSGPIFDYNYDGHFDAPDEITKHLANTDVPIPTHYFVVLTSCKNKS 300

Query: 792 HTPENCPGWLDVLPFIIPHRPTNVESCPEGKPEALWVEERFTAHIARVRDVELLTGLDFY 851
           HTPENCPGWLDVLPFIIPHRPTNVESCPEGKPEALWVEERFTAHIARVRDVELLTGLDFY
Sbjct: 301 HTPENCPGWLDVLPFIIPHRPTNVESCPEGKPEALWVEERFTAHIARVRDVELLTGLDFY 360

Query: 852 QDKVQPVSEILQLKTYLPTFETTI 875
           QDKVQPVSEILQLKTYLPTFET I
Sbjct: 361 QDKVQPVSEILQLKTYLPTFETPI 384
```

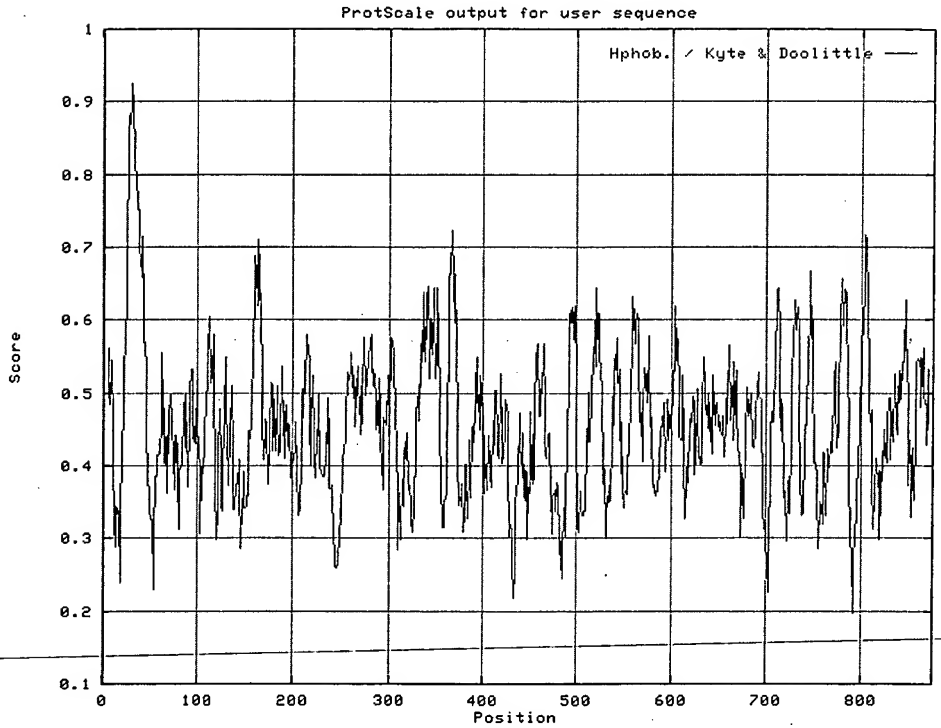
# Figure 5: 161P2F10B Hydrophilicity profile

(Hopp T.P., Woods K.R., 1981. Proc. Natl. Acad. Sci. U.S.A. 78:3824-3828)



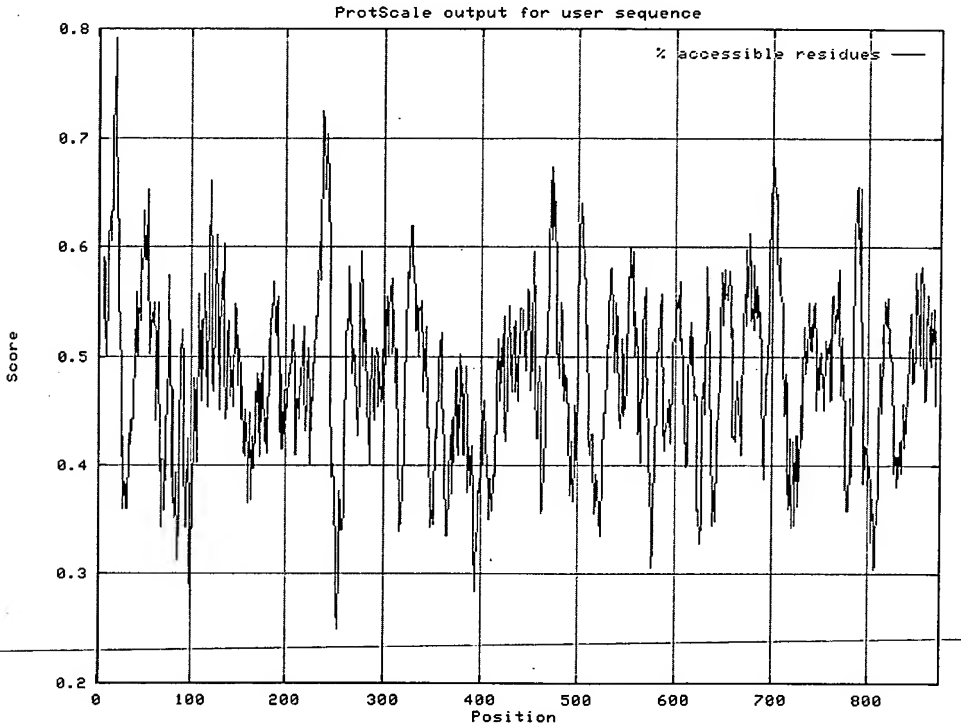
# Figure 6: 161P2F10B Hydropathicity Profile

(Kyte J., Doolittle R.F., 1982. J. Mol. Biol. 157:105-132)



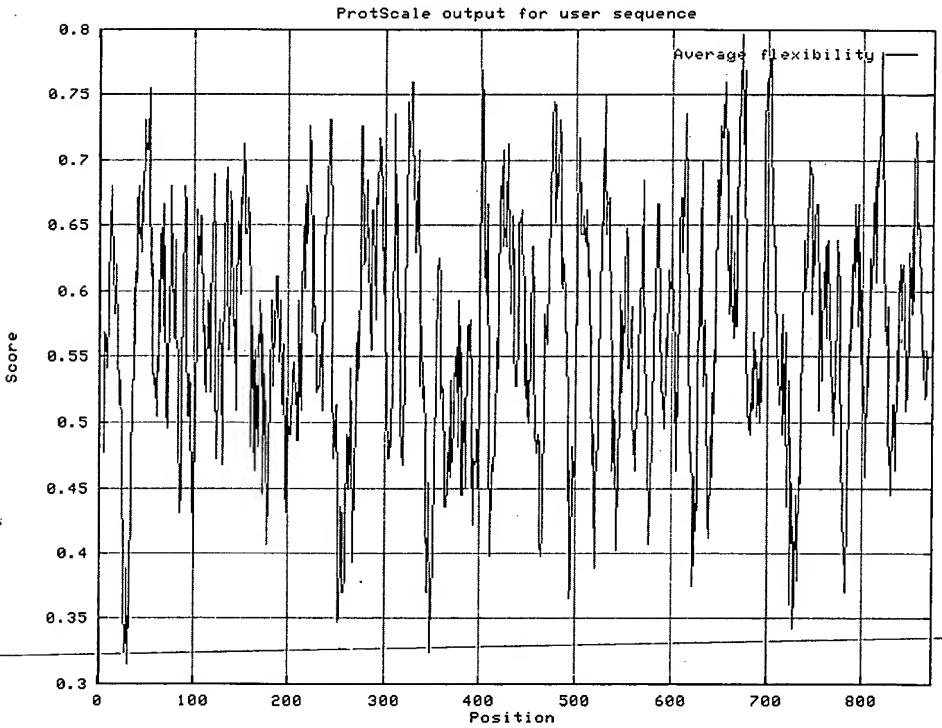
# Figure 7: 161P2F10B % Accessible Residues Profile

(Janin J., 1979. Nature 277:491-492)



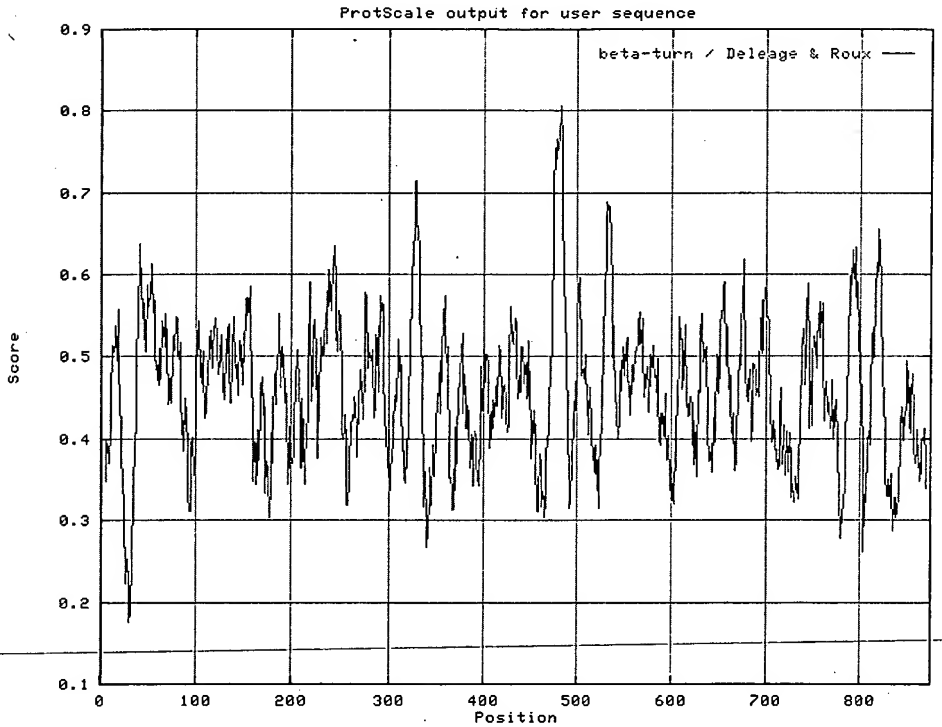
# Figure 8: 161P2F10B Average Flexibility Profile

(Bhaskaran R., Ponnuswamy P.K., 1988.
Int. J. Pept. Protein Res. 32:242-255)



# Figure 9: 161P2F10B Beta-turn Profile

(Deleage, G., Roux B. 1987. Protein Engineering 1:289-294)



# Figure 10: Expression of 161P2F10B by RT-PCR

M = Marker

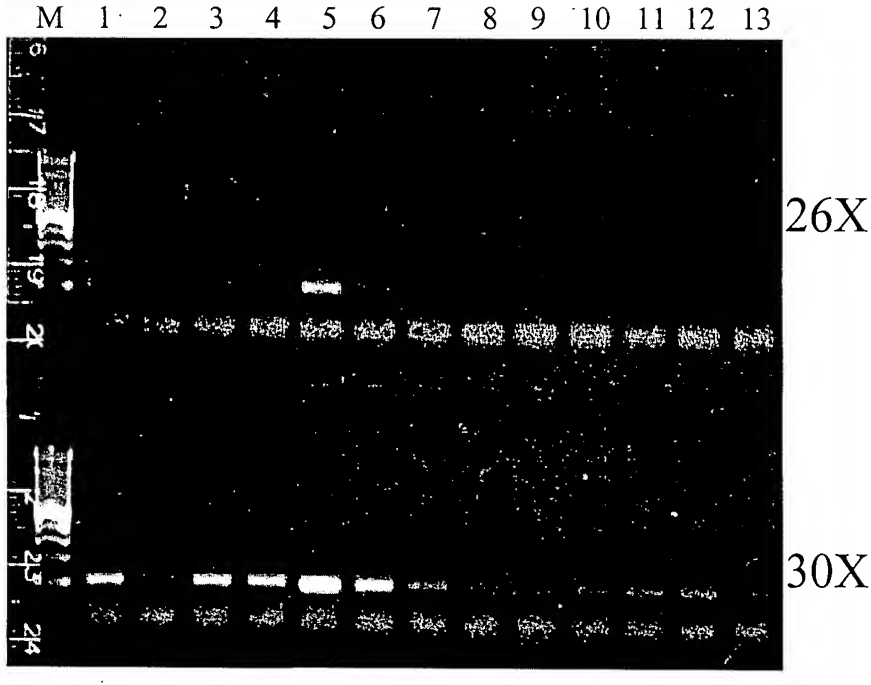
- Vital Pool 1

2) Vital Pool 2

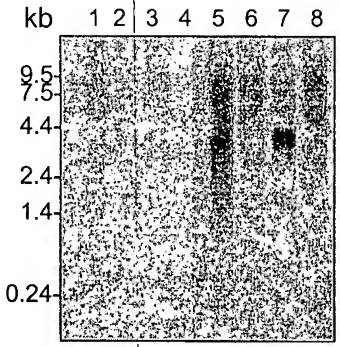
3) Xenograft Pool

4) Prostate Cancer Pool

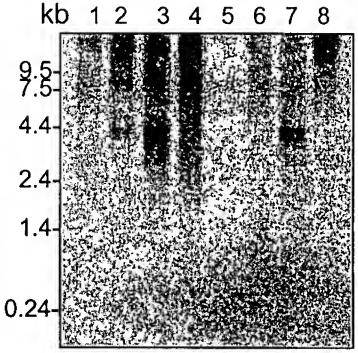
- Kidney Cancer Pool
- Colon Cancer Pool
- Lung Cancer Pool
- Ovary Cancer Pool
- Breast Cancer Pool
- Metastasis Pool
- Pancreas cancer Pool
- Prostate Met to LN #1
- Prostate Met to LN #2



# Figure 11: Expression of 161P2F10B in Normal Tissues

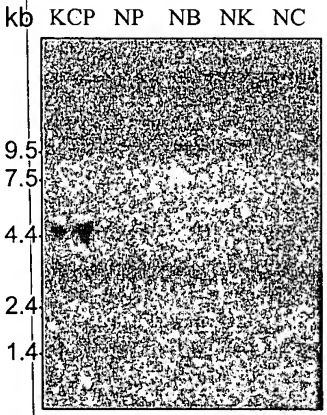



1. Heart
2. Brain
3. Placenta
4. Lung
5. Liver
6. Skeletal Muscle
7. Kidney
8. Pancreas



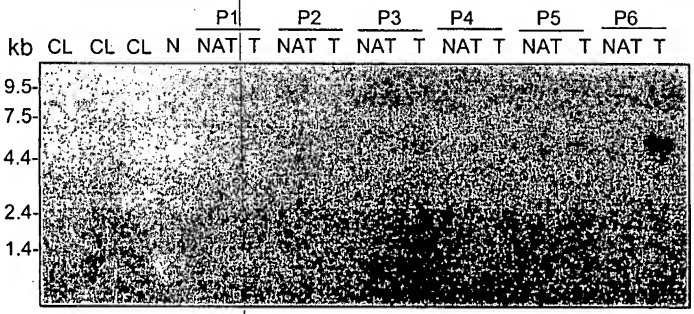

1. Spleen
2. Thymus
3. Prostate
4. Testis
5. Ovary
6. Small Intestine
7. Colon
8. Leukocytes

**Figure 12: Expression of 161P2F10B in Patient Kidney Cancer Specimens and in Normal Tissues**




*KCP = Kidney Cancer Poll*
*NP = Normal Prostate*
*NB = Normal Bladder*
*NK = Normal Kidney*
*NC = Normal Colon*

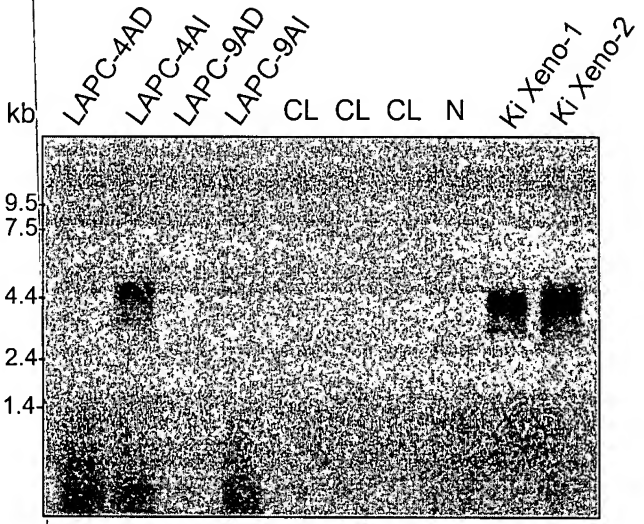
# Figure 13: Expression of 161P2F10B in Kidney Cancer Patient Specimens




CL = cell lines listed in order: 769-P, A498, SW839
N = Normal kidney
NAT = Normal adjacent tumor
T = Tumor
P = Patient

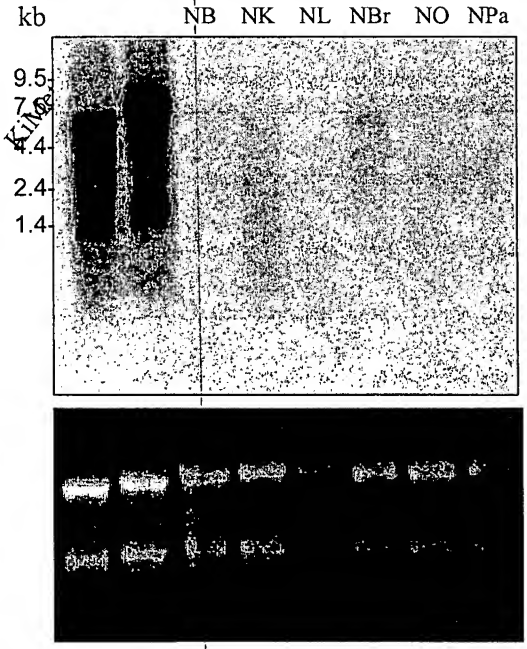
P1 - Papillary carcinoma, stage I
P2 - Invasive papillary carcinoma
P3 - Clear cell type grade 1/3, focally 2/3
P4 - Clear cell type, stage III
P5 - Clear cell type, stage III
P6 - Clear cell type, stage III

**Figure 14: Expression of 161P2F10B in Kidney Cancer Xenografts**




*CL = cell lines listed in order: 769-P, A498, Caki-1*
*N = Normal kidney*
*Ki Xeno = Kidney xenograft*

# Figure 15: Expression of 161P2F10B in Kidney Cancer Metastasis Specimens and in Normal Tissues




*KiMet 1 = Kidney Metastasis to lung*
*KiMet 2 = Kidney Metastasis to lymph node*
*NB = Normal Bladder*
*NK = Normal Kidney*
*NL = Normal Lung*
*NBr = Normal Breast*
*NO = Normal Ovary*
*NPa = Normal Pancreas*

**Figure 16: Expression of 161P2F10B Protein by Immunohistochemistry in Kidney Cancer Patient Specimens**

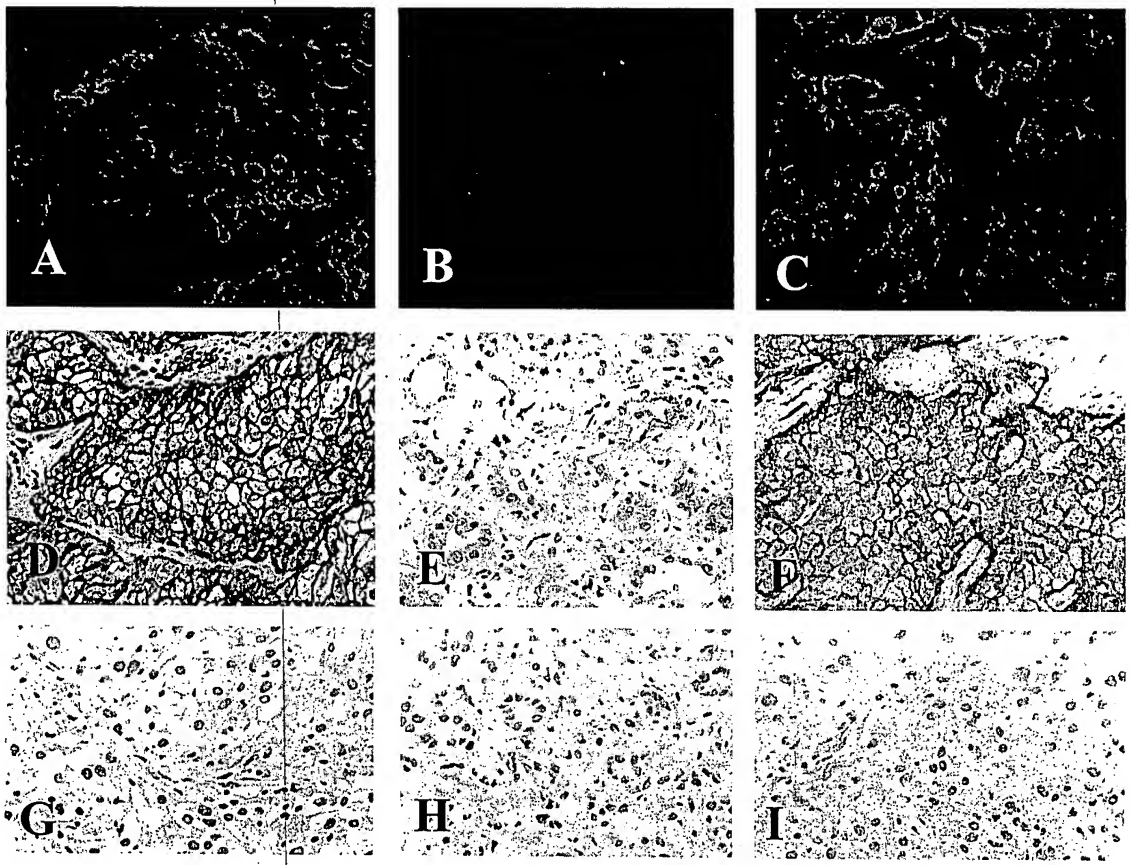


**Figure 17: Expression of 161P2F10B Protein on the Cell Surface of Renal Cell Carcinoma Xenografts**

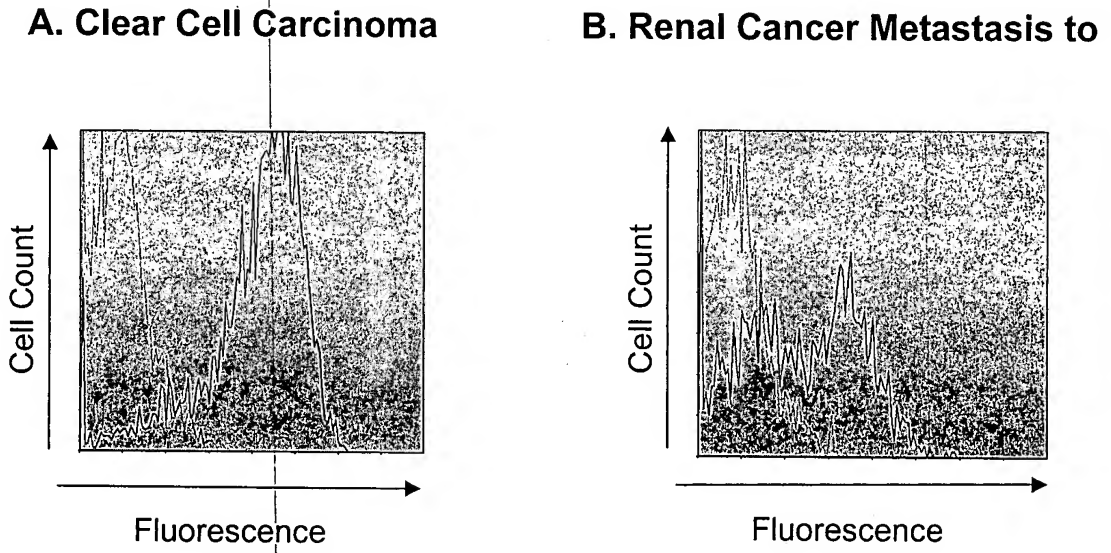
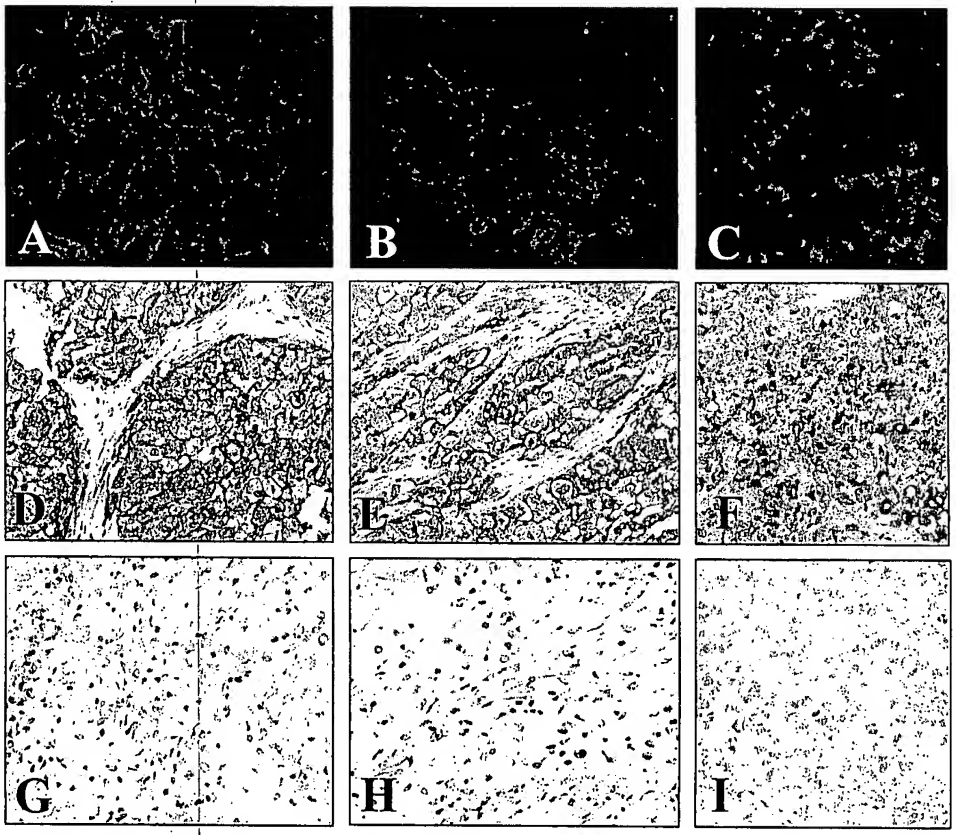


**Figure 18: Expression of 161P2F10B Protein by Immunohistochemistry in Human Cancer Xenograft Tissues**



# Figure 19A (Seq. ID. No. 751)

```
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        |         |         |         |         |         |         |
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SFPSIYMPYNGSVPFEERISTLLKWLDLPKAERPRFYTMYFEEPDSSGHAGGPVSARVIKALQVVDHAFG
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MLMEGLKQRNLHNCVNIILLADHGMDQTYCNKMEYMTDYFPRINFFYMYEGPAPRIRAHNIPHDFFSFNS
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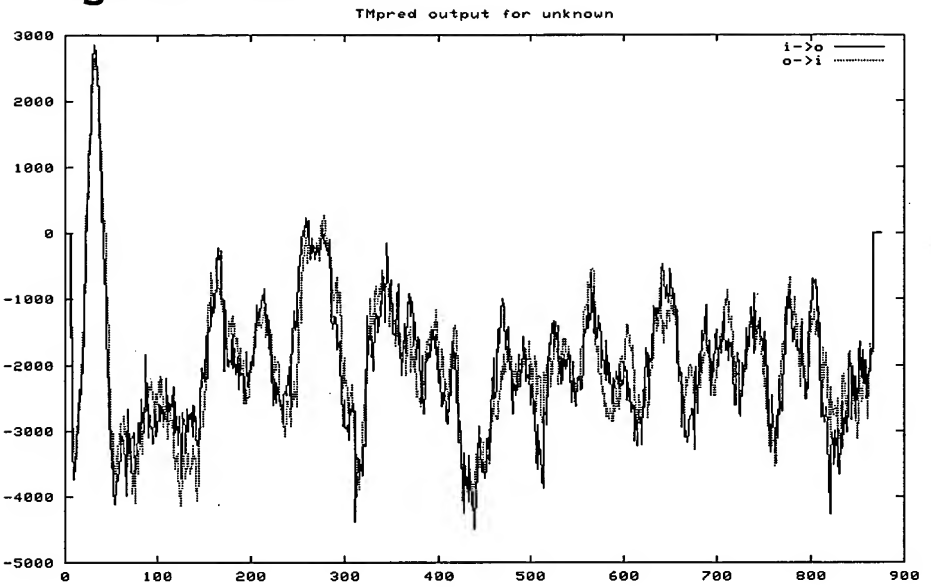
TSDSQYDALITSNLVPMYEEFRKMWDYFHSVLLIKHATERNGVNVVSGPIFDYNYDGHFDAPDEITKHLA
cchhhhhhhhhhcccchhhhhhhhhhhhhhhhhehhcccccceeeccccccccccccchhhhhhhhcc
NTDVPIPTHYFVVLTSCKNKSHTPENCPGWLDVLPFIIPHRPTNVESCPEGKPEALWVEERFTAHIARVR
ccccccceeeeeeeeccccccccccccccccceeeeccccccccccccccchhhhhhhhhhhhhhhh
DVELLTGLDFYQDKVQPVSEILQLKTYLPTFETTI
hheehccccchcchhchhhhhehhhhcccccccc
```

c: random coil (31.31%)
e: extended strand (11.31%)
h: alpha helix (57.37%)

# Figure 19B




# Figure 19C

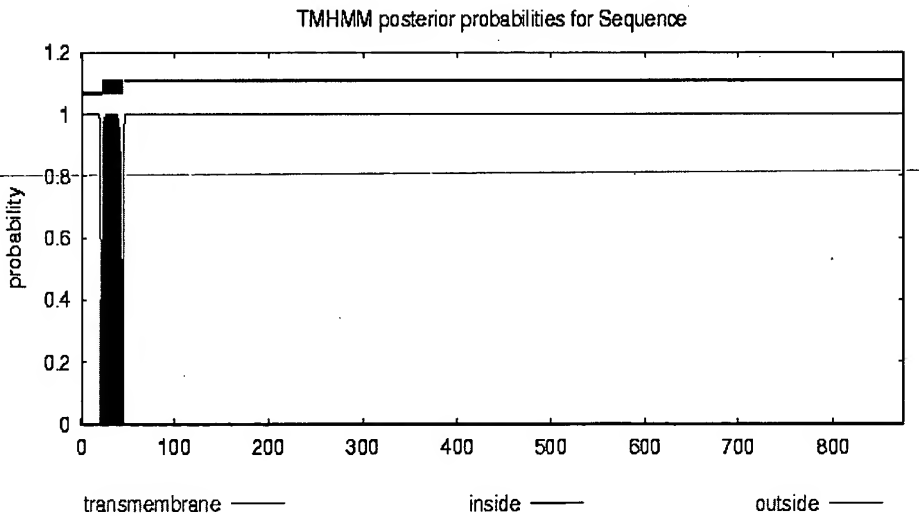
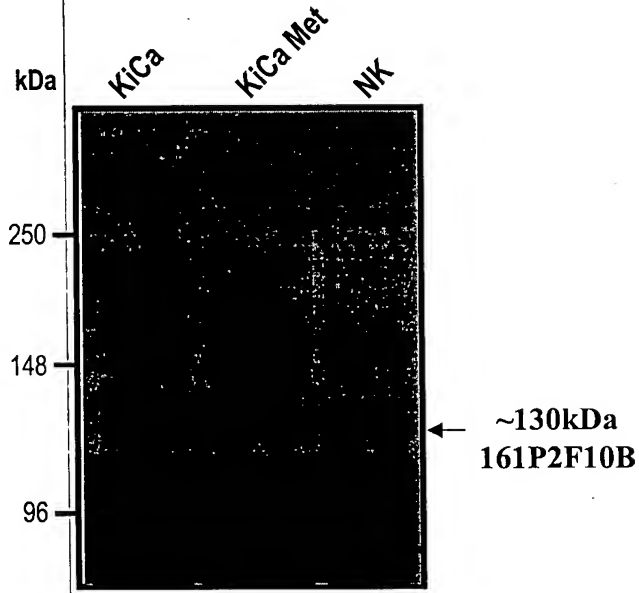
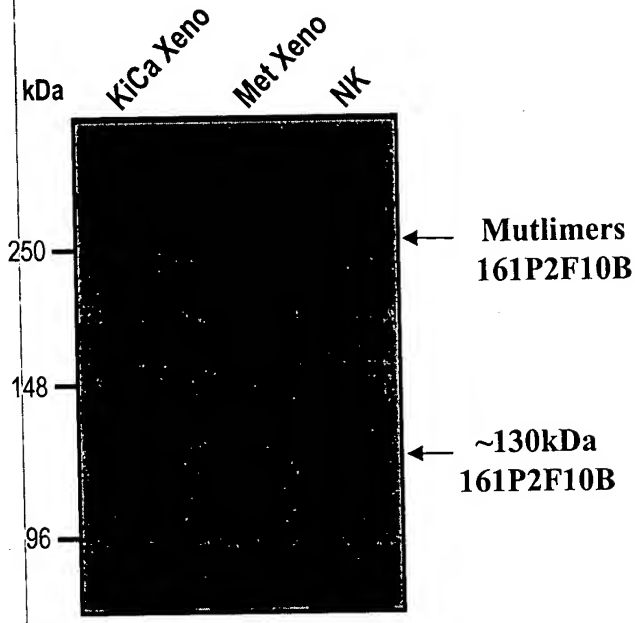


**Figure 20** Expression of 161P2F10B in Human Patient Cancers by Western Blot




*KiCa = Kidney cancer, clear cell carcinoma*
*KiCa Met = Kidney cancer metastasis to lymph node*
*NK = Normal kidney*

**Figure 21** **Expression of 161P2F10B in Human Xenograft Tissues by Western Blot**




*KiCa Xeno = Xenograft of kidney cancer, clear cell carcinoma*
*Met Xeno = Xenogrraft from Kidney cancer metastasis to lymph node*
*NK = Normal kidney*